

OIPE

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/881,823**

DATE: 07/05/2001  
 TIME: 11:17:39

Input Set : A:\PTO.txt  
 Output Set N:\CRF3\07052001\I881823.raw

3 <110> APPLICANT SHI, WENYUAN  
 4 ANDERSON, MAXWELL  
 5 MORRISON, SHERIE  
 6 TRINH, RYAN  
 7 WIMS, LETITIA  
 8 CHEN, LI  
 10 <120> TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries  
 12 <130> FILE REFERENCE: 22851-032  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/881,823  
 C--> 14 <141> CURRENT FILING DATE: 2001-06-15  
 14 <150> PRIOR APPLICATION NUMBER: US 07/378,577  
 15 <151> PRIOR FILING DATE: 1999-08-20  
 17 <160> NUMBER OF SEQ ID NOS: 32  
 19 <170> SOFTWARE: PatentIn version 3.0  
 21 <210> SEQ ID NO 1  
 22 <211> LENGTH: 420  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Murine  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION (14)..(415)  
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 32 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu  
 33 1 5 10  
 35 ctc tgg gtt cca ggt tcc aca ggt gac att gtg ctg acc caa tct cca 97  
 36 Leu Trp Val Pro Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro  
 37 15 20 25  
 39 gtt tct ttg gct gtg tct cta ggg cag agg gcc acc ata tcc tgc aga 145  
 40 Val Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg  
 41 30 35 40  
 43 gcc agt gaa agt gtt gat agt tat ggc aat agt ttt atg aac tgg tac 193  
 44 Ala Ser Glu Ser Val Asp Ser Tyr Gly Asn Ser Phe Met Asn Trp Tyr  
 45 45 50 55 60  
 47 cag cag aaa cca gga cag cca ccc caa ctc ctc atc tat cgt gca tcc 241  
 48 Gln Gln Lys Pro Gly Gln Pro Pro Gln Leu Ile Tyr Arg Ala Ser  
 49 65 70 75  
 51 aat cta gaa tac ggg atc cct gcc agg ttc agt ggc agt ggg tct agg 289  
 52 Asn Leu Glu Tyr Gly Ile Pro Ala Arg Phe Ser Gly Ser Arg  
 53 80 85 90  
 55 aca gac ttc acc ctc acc att aat cct gtg gag gct gat gat gtt gca 337  
 56 Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala  
 57 95 100 105  
 59 acc tat tac tgt cag caa aat aat gcg gat cct ccc acg ttc gga ggg 385  
 60 Thr Tyr Tyr Cys Gln Gln Asn Asn Ala Asp Pro Pro Thr Phe Gly Gly  
 61 110 115 120  
 63 ggg acc aag ttg gaa atc aaa cgt aag tcg acgct 420

**ENTERED**  
*see page 5*

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Input Set : A:\PTO.txt  
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64 Gly Thr Lys Leu Glu Ile Lys Arg Lys Ser  
65 125 130  
68 <210> SEQ ID NO: 2  
69 <211> LENGTH: 134  
70 <212> TYPE: PRT  
71 <213> ORGANISM: Murine  
73 <400> SEQUENCE: 2  
75 Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
76 1 5 10 15  
79 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Val Ser Leu Ala  
80 20 25 30  
83 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser  
84 35 40 45  
87 Val Asp Ser Tyr Gly Asn Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro  
88 50 55 60  
91 Gly Gln Pro Pro Gln Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Tyr  
92 65 70 75 80  
95 GLY Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr  
96 85 90 95  
99 Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys  
100 100 105 110  
103 Gln Gln Asn Asn Ala Asp Pro Pro Thr Phe Gly Gly Thr Lys Leu  
104 115 120 125  
107 Glu Ile Lys Arg Lys Ser  
108 130  
111 <210> SEQ ID NO: 3  
112 <211> LENGTH: 454  
113 <212> TYPE: DNA  
114 <213> ORGANISM: Murine  
116 <220> FEATURE:  
117 <221> NAME/KEY: CDS  
118 <222> LOCATION: (14)..(430)  
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122 Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr  
123 1 5 10  
125 ttc cca agc tgt gtc ctg tcc cag gtg cag ctg aag gag tca gga cct 97  
126 Phe Pro Ser Cys Val Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro  
127 15 20 25  
129 ggc ctg gtg gcg ccc tca cag agc ctg tcc atc aca tgc act gtc tca 145  
130 Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser  
131 30 35 40  
133 ggg ttc tca tta acc aac tat gat ata aat tgg gtt cgc cag cct cca 193  
134 Gly Phe Ser Leu Thr Asn Tyr Asp Ile Asn Trp Val Arg Gln Pro Pro  
135 45 50 55 60  
137 gga aag ggt ctg gag tgg ctg gga ata ata tgg qgt gac ggg agc aca 241  
138 Gly Lys Gly Leu Glu Trp Leu Gly Ile Ile Trp Gly Asp Gly Ser Thr  
139 65 70 75  
141 aat tat cat tca gct ctc ata tcc aga ctg agc atc agc aag gat aac 289

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**DATE: 07/05/2001**  
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**Input Set : A:\PTO.txt**  
**Output Set: N:\CRF3\07052001\I881823.raw**

142 Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn		
143 80 85 90		
145 tcc aag agc caa att ttc tta aaa ctg aac agt ctg caa act gat gac	337	
146 Ser Lys Ser Gln Ile Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp		
147 95 100 105		
149 aca gcc acg tac tac tgt aac tac ccg tgt tta tat ttc tat ggt atg	385	
150 Thr Ala Thr Tyr Tyr Cys Asn Tyr Pro Cys Leu Tyr Phe Tyr Gly Met		
151 110 115 120		
153 gac tac tgg ggt caa gga acc tca gtc acc gtc tct tca gct agc	430	
154 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser		
155 125 130 135		
157 acaaacagcccc catcagtgcga cccca	454	
160 <210> SEQ ID NO: 4		
161 <211> LENGTH: 139		
162 <212> TYPE: PRT		
163 <213> ORGANISM: Murine		
165 <400> SEQUENCE: 4		
167 Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys		
168 1 5 10 15		
171 Val Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala		
172 20 25 30		
175 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu		
176 35 40 45		
179 Thr Asn Tyr Asp Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu		
180 50 55 60		
183 Glu Trp Leu Gly Ile Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser		
184 65 70 75 80		
187 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln		
188 85 90 95		
191 Ile Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr		
192 100 105 110		
195 Tyr Cys Asn Tyr Pro Cys Leu Tyr Phe Tyr Gly Met Asp Tyr Trp Gly		
196 115 120 125		
199 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser		
200 130 135		
203 <210> SEQ ID NO: 5		
204 <211> LENGTH: 411		
205 <212> TYPE: DNA		
206 <213> ORGANISM: Murine		
208 <220> FEATURE:		
209 <221> NAME/KEY: CDS		
210 <222> LOCATION: (14)..(406)		
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214 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu		
215 1 5 10		
217 atc agt gtc aca gtc ata ttg acc aat gga gaa att ttg ctc acc ccg	97	
218 Ile Ser Val Thr Val Ile Leu Thr Asn Gly Glu Ile Leu Leu Thr Pro		
219 15 20 25		

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221	tct	cca	gca	atc	ata	gct	gca	tct	cct	ggg	gaa	aag	gtc	acc	atc	acc	145
222	Ser	Pro	Ala	Ile	Ile	Ala	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	
223	30				35						40						
225	tgc	agt	gcc	agc	tca	agt	gtt	agt	tac	atg	aac	tgg	tac	cag	cag	aaa	193
226	Cys	Ser	Ala	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys		
227	45				50					55			60				
229	cca	gga	tct	tcc	ccc	aaa	atc	tgg	att	tat	ggt	gtt	tcc	aac	ctg	gct	241
230	Pro	Gly	Ser	Ser	Pro	Lys	Ile	Trp	Ile	Tyr	Gly	Val	Ser	Asn	Leu	Ala	
231							65			70			75				
233	tct	gga	gtt	cct	gtc	tgc	ttc	agt	ggc	agt	ggg	tct	ggg	aca	tct	ttc	289
234	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Phe	
235							80			85			90				
237	tct	ttc	aca	atc	aac	agc	atg	gag	gtc	gaa	gat	gtt	gcc	act	tat	tac	337
238	Ser	Phe	Thr	Ile	Asn	Ser	Met	Glu	Ala	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	
239							95			100			105				
241	tgt	cag	caa	agg	agt	agt	tac	cca	ttc	acg	ttc	ggc	tcg	ggg	acc	aag	385
242	Cys	Gln	Gln	Arg	Ser	Ser	Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	
243							110			115			120				
245	ctg	gaa	ata	aaa	cgt	aag	tgc	acgt									411
246	Leu	Glu	Ile	Lys	Arg	Lys	Ser										
247	125				130												
250	<210>	SEQ ID NO:	6														
251	<211>	LENGTH:	131														
252	<212>	TYPE:	PRT														
253	<213>	ORGANISM:	Murine														
255	<400>	SEQUENCE:	6														
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258	1				5				10					15			
261	Val	Ile	Leu	Thr	Asn	Gly	Glu	Ile	Leu	Leu	Thr	Pro	Ser	Pro	Ala	Ile	
262							20			25			30				
265	Ile	Ala	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	
266							35			40			45				
269	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	
270						50			55			60					
273	Pro	Lys	Ile	Trp	Ile	Tyr	Gly	Val	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	
274						65			70			75			80		
277	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Phe	Ser	Phe	Thr	Ile	
278						85				90			95				
281	Asn	Ser	Met	Glu	Ala	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	
282						100				105			110				
285	Ser	Ser	Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
286						115				120			125				
289	Arg	Lys	Ser														
290			130														
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294	<211>	LENGTH	465														
295	<212>	TYPE:	DNA														
296	<213>	ORGANISM:	Murine														
298	<220>	FEATURE:															

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TIME: 11:17:40

Input Set : A:\PTO.txt  
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299 <221> NAME/KEY: CDS  
 300 <222> LOCATION: (13)..(441)  
 302 <400> SEQUENCE: 7  
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       Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Ile Val  
 304           1           5           10  
 305            15          20          25  
 306 ctc gca tat gtc ctc tcc cag gtt act ctg aaa gag tct ggc cct ggg 99  
 307 Pro Ala Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly  
 308           15          20          25  
 309            35          40          45  
 310 ata ttg cag ccc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg 147  
 311 Ile Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly  
 312           35          40          45  
 313 ttt tca ctg aga act tat ggt ata gga gta ggc tgg att cgt cag cct 195  
 314 Phe Ser Leu Arg Thr Tyr Gly Ile Gly Val Gly Trp Ile Arg Gln Pro  
 315           50          55          60  
 316 tca ggg agg ggt ctg gag tgg ctg gca cac att tgg tgg aat gat aat 243  
 317 Ser Gly Arg Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asn Asp Asn  
 318           65          70          75  
 319 aug tac tat aac aca gtc ctg aag agc cgg ctc aca atc tcc aag gat 291  
 320 Lys Tyr Tyr Asn Thr Val Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp  
 321           80          85          90  
 322 acc tcc aac aac cag gta ttc ctc aag atc gcc agt gtg gac act gca 339  
 323 Thr Ser Asn Asn Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala  
 324           95          100        105  
 325 qat act gcc aca tac tac tgt gcg cga ata gag ggg ggc tcg ggc tac 387  
 326 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Glu Gly Ser Gly Tyr  
 327           110        115        120        125  
 328 qat gtt atg gac tac tgg ggt caa gga atc tca gtc acc gtc tct tca 435  
 329 Asp Val Met Asp Tyr Trp Gly Gln Gly Ile Ser Val Thr Val Ser Ser  
 330           130        135        140  
 331 qct agc acaacacccc catctgtcga cccca 465  
 340 Ala Ser  
 341 <210> SEQ ID NO: 8  
 342 <211> LENGTH: 143  
 343 <212> TYPE: PRT  
 344 <213> ORGANISM: Murine  
 345 <400> SEQUENCE: 8  
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 348 1            15  
 349 Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln  
 350           20          25        30  
 351 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu  
 352           35          40        45  
 353 Arg Thr Tyr Gly Ile Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Arg  
 354           50          55        60  
 355 Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr  
 356           65          70        75        80  
 357 Asn Thr Val Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn  
 358           85          90        95

FYI.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/881,823

DATE 07/05/2001  
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Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07052001\I881823.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L.14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L.637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L 641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17